

REMARKS

Applicants have cancelled claim 38.

Applicants have amended claims 23, 24, and 27 to delete the term “approximately”. Support for this amendment can be found throughout the specification, and particularly, for example, on page 2, lines 24-28, page 4, lines 3-9, and page 9, lines 20-25.

Applicants have amended claims 23, 27, and 43 to include the sequence identifier (SEQ ID NO:1) for the amino acid sequence of the tandem repeat unit and SEQ ID NO:2, the nucleic acid encoding the tandem repeat. Support for the amendment can be found throughout the specification, and particularly, for example on page 4, lines 10-19, page 2, lines 8-11, and page 10, lines 8-31.

Applicants have also amended claims 23, 27, and 43 to specifically define that the nucleic acid alteration is intended to encompass wobbling in at least one of the nucleic acid sequences encoding the 5-25 MUC1 repeats while retaining the amino acid sequence of the native tandem repeat pattern of SEQ ID NO:1. Specific support for this amendment can be found, for example, on page 10, lines 23-30, page 4, lines 10-19, page 2, lines 8-11, and page 10, lines 8-31.

Thus the amendments to the claims are supported by the specification and do not introduce new matter. Entry of the amended claims is respectfully requested.

Applicants have added new claims 60-63. These claims are directed to embodiments including wobbled MUC1 repeats presented in Table A, on page 11, (Claims 60-61), and embodiments encompassing sequences, wherein the amino acids in the MUC1 repeat are substituted with a conservative amino acid including glycine/serine and leucine/valine substitutions, which are disclosed, for example, at page 10, lines 2-7. Therefore, no new matter has been added by introducing these claims and their entry is respectfully requested.

New claim 64 is directed to a recombinant pox virus comprising a nucleic acid sequence encoding an immunogenic MUC1 fragment comprising 6 identical tandem repeat units. The application provides a range of 5-25 tandem repeat unit. See, page 4, line 4. Thus, the

application clearly provides support for any member of the range. *In re Wertheim*, 541 F.2d 257, 192 USPQ 90 (CCPA 1976).

Turning now to the specific rejections.

Claim 38 was rejected under 35 U.S.C. §112, first paragraph. Applicants have cancelled claim 38 to expedite prosecution, and thus the rejections are moot.

Claims 23-51 were rejected under 35 U.S.C. §112, second paragraph because they recited to term “approximately.” Examiner further contends that the phrase “wherein said nucleic acid is altered from the native tandem repeat pattern” is not clear.

To expedite prosecution, applicants have amended the claims by removing the term “approximately.” While applicants respectfully submit that the phrase “wherein said nucleic acid is altered from the native tandem repeat pattern of SEQ ID NO:1” should be clear in light of the specification, applicants have amended the claims to read that “the nucleic acid sequence is altered from the nucleic acid sequence of SEQ ID NO:2 by using wobbled codons to reduce homology between the tandem repeats while retaining amino acid sequence SEQ ID NO:1”. (Page 9, lines 30-32, page 10, lines 8-28). Applicants respectfully submit that “wobbling” or “wobble” is a term well known to those in the art (see, e.g., Exhibit A which is a copy of p. 744 and cover pages of *Biochemistry*, Third edition, Ed. Stryer L., W.H. Freeman and Company, New York, NY, 1988). SEQ ID NO:1 clearly defines what the amino acid sequence is and because wobbling is a defined term, one skilled in the art will know what sequence variations are encompassed by the claim. Therefore, applicants submit that the amended claim allows one skilled in the art to clearly determine the claimed subject matter and thus request that the rejections under 35 U.S.C. §112, second paragraph be withdrawn.

Claims 23-25 and 27 were rejected under 35 U.S.C. §102(b) over Acres et al. (“Acres”).

Claims have been amended to require at least 5 repeats. Acres does not teach use of more than 4 repeats, therefore, the required elements of the claims are not taught by Acres. Therefore, applicants respectfully submit that the rejection under 35 U.S.C. §102(b) over Acres be withdrawn.

Claims 23-37 and 9-59 were rejected under 35 U.S.C. §103(a) over Acres in view of Paoletti (U.S. Patent No. 5,942,235) and Gunaburg et al. ("Gunaburg").

To show *prima facie* case of obviousness the combination of references must teach all the elements of the claims (MPEP 2143). As discussed above, the claims have been amended to require that at least 5 repeats are used. Because Acres only shows use of 3 to 4 repeats, and neither Paoletti nor Gunaburg teach using MUC repeats, not to mention the more than 4 repeats, the required elements of the claims are not taught by the combination of these references. Therefore applicants respectfully submit that the rejections under 35 U.S.C. §103(a) be withdrawn.

In the event that there are any questions relating to this Amendment or to the application in general, it is kindly requested that the Examiner contact the undersigned attorney concerning the same to expedite prosecution of this application.

Applicants believe no fees are currently due. In the event a fee is due in connection with this submission, the Commissioner is herewith authorized to charge Nixon Peabody LLP Deposit Account No. 50-0850.

Entry of the foregoing amendment and prompt and favorable consideration of the application is respectfully requested.

Date: November 5, 2004

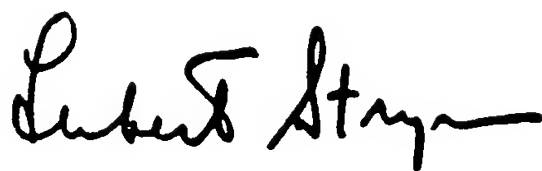
Respectfully submitted,



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mally contained cysteine but not alanine. On the other hand, peptides normally containing alanine but not cysteine were devoid of radioactivity. Thus, *the amino acid in aminoacyl-tRNA does not play a role in selecting a codon.*

SOME TRANSFER RNA MOLECULES RECOGNIZE MORE THAN ONE CODON BECAUSE OF WOBBLE IN BASE PAIRING

What are the rules that govern the recognition of a codon by the anticodon of a tRNA? A simple hypothesis is that each of the bases of the codon forms a Watson-Crick type of base pair with a complementary base on the anticodon. The codon and anticodon would then be lined up in an antiparallel fashion. In the accompanying diagram at the left, the prime denotes the complementary base. Thus X and X' would be either A and U (or U and A) or G and C (or C and G). A specific prediction of this model is that a particular anticodon can recognize only one codon.

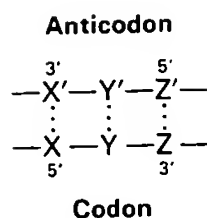


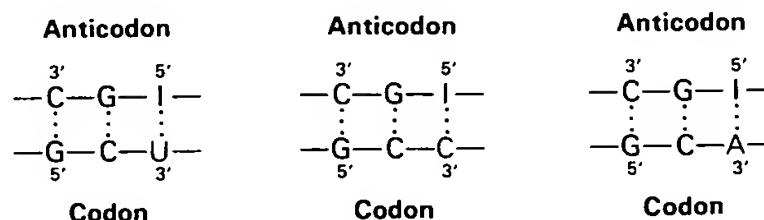
Table 30-3

Allowed pairings at the third base of the codon according to the wobble hypothesis

First base of anticodon	Third base of codon
C	G
A	U
U	A or G
G	U or C
I	U, C, or A

The facts are otherwise. *Some pure tRNA molecules can recognize more than one codon.* For example, the yeast alanine tRNA studied by Holley binds to *three* codons: GCU, GCC, and GCA. The first two bases of these codons are the same, whereas the third is different. Could it be that the recognition of the third base of a codon is sometimes less discriminating than recognition of the other two? The pattern of degeneracy of the genetic code indicates that this might be so. XYU and XYG always code for the same amino acid, whereas XYA and XYG usually do. Crick surmised from these data that the steric criteria for pairing of the third base might be less stringent than for the other two. Models of various base pairs were built to determine which ones are similar to the standard AU and GC base pairs with regard to the distance and angle between the glycosidic bonds. Inosine was included in this study because it appeared in several anticodons. Assuming some steric freedom ("wobble") in the pairing of the third base of the codon, the combinations shown in Table 30-3 seemed plausible.

The wobble hypothesis is now firmly established. The anticodons of tRNAs of known sequence bind to the codons predicted by this hypothesis. For example, the anticodon of yeast alanine tRNA is IGC. This tRNA recognizes the codons GCU, GCC, and GCA. Recall that, by convention, nucleotide sequences are written in the 5' → 3' direction unless otherwise noted.



Thus, I pairs with U, C, or A, as predicted. Phenylalanine tRNA, which has the anticodon GAA, recognizes the codons UUU and UUC but not UUA and UUG.

